

30 CGCCCAGCCGCCCCCCAAGCCCCTGAGGTTTCCGGGGACCACAATGAACAAGTTGCTG MNKL 110 TGCTGCGCGCTCGTGTTTCTGGACATCTCCATTAAGTGGACCACCCAGGAAACGTTTCCT C A L V F L D I S I K W T T O E T F P 170 150 CCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTGTGTGACAAATGTCCT KYLHYDEETSHQLLCDKCP 210 CCTGGTACCTACAAAACAACACTGTACAGCAAAGTGGAAGACCGTGTGCGCCCCTTGC P G T Y L K Q H C T A K W K T V C A P C 270 290 250 CCTGACCACTACTACACAGACAGCTGGCACACCAGTGACGAGTGTCTATACTGCAGCCCC PDHYYTDSWHTSDECLYCSP 350 330 GTGTGCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACCCACAACCGCGTGTGC V C K E L Q Y V K Q E C N R T H N R V C 410 390 370 GAATGCAAGGAAGGCGCTACCTTGAGATAGAGTTCTGCTTGAAACATAGGAGCTGCCCT ECKEGRYLEIEFCLKHRSCP 470 450 CCTGGATTTGGAGTGGTGCAAGCTGGAACCCCAGAGCGAAATACAGTTTGCAAAAGATGT P G F G V V Q A G T P E R N T V C K R C 510 490 CCAGATGGGTTCTTCTCAAATGAGACGTCATCTAAAGCACCCTGTAGAAAACACACAAAT D G F F S N E T S S K A P C R K H T N 590 570 SVFGLLLTQKGNATHDNIC 630 650 610 TCCGGAAACAGTGAATCAACTCAAAAATGTGGAATAGATGTTACCCTGTGTGAGGAGGCA S G N S E S T Q K C G I D V T L C E E A 710 690 TTCTTCAGGTTTGCTGTTCCTACAAAGTTTACGCCTAACTGGCTTAGTGTCTTGGTAGAC FRFAVPTKFTPNWLSVLVD 750 AATTTGCCTGGCACCAAAGTAAACGCAGAGAGTGTAGAGAGGATAAAACGGCAACACAGC NLPGTKVNAESVERIKRQHS 810 TCACAAGAACAGACTTTCCAGCTGCTGAAGTTATGGAAACATCAAAACAAAGACCAAGAT SQEQTFQLLKLWKHQNKDQD 870 ATAGTCAAGAAGATCATCCAAGATATTGACCTCTGTGAAAACAGCGTGCAGCGGCACATT I V K K I I Q D I D L C E N S V Q R H I 950 930 GGACATGCTAACCTCACCTTCGAGCAGCTTCGTAGCTTGATGGAAAGCTTACCGGGAAAG G H A N L T F E Q L R S L M E S L P G K 990 1010 970 AAAGTGGGAGCAGAAGACATTGAAAAAACAATAAAGGCATGCAAACCCAGTGACCAGATC K V G A E D I E K T I K A C K P S D Q I 1050 1070 1030 CTGAAGCTGCTCAGTTTGTGGCGAATAAAAAATGGCGACCAAGACACCTTGAAGGGCCTA K L L S L W R I K N G D Q D T L K G L 1110 1130 ATGCACGCACTAAAGCACTCAAAGACGTACCACTTTCCCAAAACTGTCACTCAGAGTCTA



V T Q S L MHALKHSKTYHF ${\tt AAGAAGACCATCAGGTTCCTTCACAGCTTCACAATGTACAAATTGTATCAGAAGTTATTT}$ K K T I R F L H S F T M Y K L Y Q K L F TTAGAAATGATAGGTAACCAGGTCCAATCAGTAAAAATAAGCTGCTTATAACTGGAAATG GCCATTGAGCTGTTTCCTCACAATTGGCGAGATCCCATGGATGAGTAAACTGTTTCTCAG GCACTTGAGGCTTTCAGTGATATCTTTCTCATTACCAGTGACTAATTTTGCCACAGGGTA CTAAAAGAAACTATGATGTGGAGAAAGGACTÄACATCTCCTCCAATAAACCCCAAATGGT TAATCCAACTGTCAGATCTGGATCGTTATCTACTGACTATATTTTCCCTTATTACTGCTT GCAGTAATTCAACTGGAAAAAAAAAA



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1	MNKLLCCALVFLDISIKWTTQETFPPKYLHYDEETS	36
1	: ::: : . . :: MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTA	50
37	HOLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPV : . : : .	86
51	.QMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSR	99
87	CKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGV	130
100	. . .: : .: .:. : . . CSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGV	149
131	VQAGTPERNTVCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNAT	180
	ARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNAS	195
181	HDNICSGNSESTQKCGIDVTLCEEAFF	207
196	.: : : MDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPM	245
208		242
246	GPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLC	293
243	.QHSSQEQTFQLLKLWKHQNKDQDIVKKIIQDIDLCENSVQRHIG	286
294	:: : : ::: :: :	343
287	HANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKPSDQILKLLSLWR	333
344	. .:: . : : .: .: TRNQPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSS	391
334	IKNGDQDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMY	378
392	.:::::::::::::::::::::::::::::::::::	441
379	KLYQKLFLEMIGNQVQSVKISCL. 401 :. .: ::	
442	GSTEEKPLPL.GVPDAGMKPS 461	